

RAW SEQUENCE LISTING

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Application Serial Number: 10/S16, S17

Source: PCT

Date Processed by STIC: 12-10-04

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PCT

RAW SEQUENCE LISTING

DATE: 12/10/2004

PATENT APPLICATION: US/10/516,517

TIME: 14:26:34

Input Set : A:\Q85059.txt

Output Set: N:\CRF4\12102004\J516517.raw

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3 <110> APPLICANT: Yamanouchi Pharmaceutical Co.,Ltd.
4     Kentaro ENJO
5     Sadao KUROMITSU
7 <120> TITLE OF INVENTION: Method for screening an agent for treating renal failure
9 <130> FILE REFERENCE: Q85059
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/516,517
C--> 11 <141> CURRENT FILING DATE: 2004-12-02
11 <150> PRIOR APPLICATION NUMBER: PCT/JP03/012967
12 <151> PRIOR FILING DATE: 2003-10-09
14 <150> PRIOR APPLICATION NUMBER: JP2002-298958
15 <151> PRIOR FILING DATE: 2002-10-11
17 <160> NUMBER OF SEQ ID NOS: 20
19 <170> SOFTWARE: PatentIn version 3.1
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 993
23 <212> TYPE: DNA
24 <213> ORGANISM: Homo sapiens
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (1)..(990)
29 <223> OTHER INFORMATION: inventor:Enjo, Kentaro; Kuromitsu, Sadao
32 <400> SEQUENCE: 1
33 atg gca tgg aat gca act tgc aaa aac tgg ctg gca gca gag gct gcc      48
34 Met Ala Trp Asn Ala Thr Cys Lys Asn Trp Leu Ala Ala Glu Ala Ala
35 1          5          10          15
37 ctg gaa aag tac tac ctt tcc att ttt tat ggg att gag ttc gtt gtg      96
38 Leu Glu Lys Tyr Tyr Leu Ser Ile Phe Tyr Gly Ile Glu Phe Val Val
39          20          25          30
41 gga gtc ctt gga aat acc att gtt gtt tac ggc tac atc ttc tct ctg      144
42 Gly Val Leu Gly Asn Thr Ile Val Val Tyr Gly Tyr Ile Phe Ser Leu
43          35          40          45
45 aag aac tgg aac agc agt aat att tat ctc ttt aac ctc tct gtc tct      192
46 Lys Asn Trp Asn Ser Ser Asn Ile Tyr Leu Phe Asn Leu Ser Val Ser
47          50          55          60
49 gac tta gct ttt ctg tgc acc ctc ccc atg ctg ata agg agt tat gcc      240
50 Asp Leu Ala Phe Leu Cys Thr Leu Pro Met Leu Ile Arg Ser Tyr Ala
51 65          70          75          80
53 aat gga aac tgg ata tat gga gac gtg ctc tgc ata agc aac cga tat      288
54 Asn Gly Asn Trp Ile Tyr Gly Asp Val Leu Cys Ile Ser Asn Arg Tyr
55          85          90          95
57 gtg ctt cat gcc aac ctc tat acc agc att ctc ttt ctc act ttt atc      336
58 Val Leu His Ala Asn Leu Tyr Thr Ser Ile Leu Phe Leu Thr Phe Ile
59          100          105          110

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61 agc ata gat cga tac ttg ata att aag tat cct ttc cga gaa cac ctt      384
62 Ser Ile Asp Arg Tyr Leu Ile Ile Lys Tyr Pro Phe Arg Glu His Leu
63      115      120      125
65 ctg caa aag aaa gag ttt gct att tta atc tcc ttg gcc att tgg gtt      432
66 Leu Gln Lys Lys Glu Phe Ala Ile Leu Ile Ser Leu Ala Ile Trp Val
67      130      135      140
69 tta gta acc tta gag tta cta ccc ata ctt ccc ctt ata aat cct gtt      480
70 Leu Val Thr Leu Glu Leu Leu Pro Ile Leu Pro Leu Ile Asn Pro Val
71      145      150      155      160
73 ata act gac aat ggc acc acc tgt aat gat ttt gca agt tct gga gac      528
74 Ile Thr Asp Asn Gly Thr Thr Cys Asn Asp Phe Ala Ser Ser Gly Asp
75      165      170      175
77 ccc aac tac aac ctc att tac agc atg tgt cta aca ctg ttg ggg ttc      576
78 Pro Asn Tyr Asn Leu Ile Tyr Ser Met Cys Leu Thr Leu Leu Gly Phe
79      180      185      190
81 ctt att cct ctt ttt gtg atg tgt ttc ttt tat tac aag att gct ctc      624
82 Leu Ile Pro Leu Phe Val Met Cys Phe Phe Tyr Tyr Lys Ile Ala Leu
83      195      200      205
85 ttc cta aag cag agg aat agg cag gtt gct act gct ctg ccc ctt gaa      672
86 Phe Leu Lys Lys Gln Arg Asn Arg Gln Val Ala Thr Ala Leu Pro Leu Glu
87      210      215      220
89 aag cct ctc aac ttg gtc atc atg gca gtg gta atc ttc tct gtg ctt      720
90 Lys Pro Leu Asn Leu Val Ile Met Ala Val Val Ile Phe Ser Val Leu
91      225      230      235      240
93 ttt aca ccc tat cac gtc atg cgg aat gtg agg atc gct tca cgc ctg      768
94 Phe Thr Pro Tyr His Val Met Arg Asn Val Arg Ile Ala Ser Arg Leu
95      245      250      255
97 ggg agt tgg aag cag tat cag tgc act cag gtc gtc atc aac tcc ttt      816
98 Gly Ser Trp Lys Gln Tyr Gln Cys Thr Gln Val Val Ile Asn Ser Phe
99      260      265      270
101 tac att gtg aca cgg gct ttg ggc ttt ctg aac agt gtc atc aac cct      864
102 Tyr Ile Val Thr Arg Ala Leu Gly Phe Leu Asn Ser Val Ile Asn Pro
103      275      280      285
105 gtc ttc tat ttt ctt ttg gga gat cac ttc agg gac atg ctg atg aat      912
106 Val Phe Tyr Phe Leu Leu Gly Asp His Phe Arg Asp Met Leu Met Asn
107      290      295      300
109 caa ctg aga cac aac ttc aaa tcc ctt aca tcc ttt agc aga tgg gct      960
110 Gln Leu Arg His Asn Phe Lys Ser Leu Thr Ser Phe Ser Arg Trp Ala
111      305      310      315      320
113 cat gaa ctc cta ctt tca ttc aga gaa aag tga      993
114 His Glu Leu Leu Leu Ser Phe Arg Glu Lys
115      325      330
118 <210> SEQ ID NO: 2
119 <211> LENGTH: 330
120 <212> TYPE: PRT
121 <213> ORGANISM: Homo sapiens
123 <400> SEQUENCE: 2
125 Met Ala Trp Asn Ala Thr Cys Lys Asn Trp Leu Ala Ala Glu Ala Ala
126 1      5      10      15

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129 Leu Glu Lys Tyr Tyr Leu Ser Ile Phe Tyr Gly Ile Glu Phe Val Val
130          20          25          30
133 Gly Val Leu Gly Asn Thr Ile Val Val Tyr Gly Tyr Ile Phe Ser Leu
134          35          40          45
137 Lys Asn Trp Asn Ser Ser Asn Ile Tyr Leu Phe Asn Leu Ser Val Ser
138          50          55          60
141 Asp Leu Ala Phe Leu Cys Thr Leu Pro Met Leu Ile Arg Ser Tyr Ala
142 65          70          75          80
145 Asn Gly Asn Trp Ile Tyr Gly Asp Val Leu Cys Ile Ser Asn Arg Tyr
146          85          90          95
149 Val Leu His Ala Asn Leu Tyr Thr Ser Ile Leu Phe Leu Thr Phe Ile
150          100          105          110
153 Ser Ile Asp Arg Tyr Leu Ile Ile Lys Tyr Pro Phe Arg Glu His Leu
154          115          120          125
157 Leu Gln Lys Lys Glu Phe Ala Ile Leu Ile Ser Leu Ala Ile Trp Val
158          130          135          140
161 Leu Val Thr Leu Glu Leu Leu Pro Ile Leu Pro Leu Ile Asn Pro Val
162 145          150          155          160
165 Ile Thr Asp Asn Gly Thr Thr Cys Asn Asp Phe Ala Ser Ser Gly Asp
166          165          170          175
169 Pro Asn Tyr Asn Leu Ile Tyr Ser Met Cys Leu Thr Leu Leu Gly Phe
170          180          185          190
173 Leu Ile Pro Leu Phe Val Met Cys Phe Phe Tyr Tyr Lys Ile Ala Leu
174          195          200          205
177 Phe Leu Lys Gln Arg Asn Arg Gln Val Ala Thr Ala Leu Pro Leu Glu
178          210          215          220
181 Lys Pro Leu Asn Leu Val Ile Met Ala Val Val Ile Phe Ser Val Leu
182 225          230          235          240
185 Phe Thr Pro Tyr His Val Met Arg Asn Val Arg Ile Ala Ser Arg Leu
186          245          250          255
189 Gly Ser Trp Lys Gln Tyr Gln Cys Thr Gln Val Val Ile Asn Ser Phe
190          260          265          270
193 Tyr Ile Val Thr Arg Ala Leu Gly Phe Leu Asn Ser Val Ile Asn Pro
194          275          280          285
197 Val Phe Tyr Phe Leu Leu Gly Asp His Phe Arg Asp Met Leu Met Asn
198          290          295          300
201 Gln Leu Arg His Asn Phe Lys Ser Leu Thr Ser Phe Ser Arg Trp Ala
202 305          310          315          320
205 His Glu Leu Leu Leu Ser Phe Arg Glu Lys
206          325          330
209 <210> SEQ ID NO: 3
210 <211> LENGTH: 29
211 <212> TYPE: DNA
212 <213> ORGANISM: Artificial Sequence
214 <220> FEATURE:
215 <223> OTHER INFORMATION: Description of Artificial Sequence:an artificially
synthesized
216          primer sequence
218 <400> SEQUENCE: 3
219 ggtctagaat ggcattggaat gcaacttgc

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RAW SEQUENCE LISTING

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222 <210> SEQ ID NO: 4
223 <211> LENGTH: 32
224 <212> TYPE: DNA
225 <213> ORGANISM: Artificial Sequence
227 <220> FEATURE:
228 <223> OTHER INFORMATION: Description of Artificial Sequence:an artificially
synthesized
229     primer sequence
231 <400> SEQUENCE: 4
232 ggtctagatt atcacttttc tctgaatgaa ag                      32
235 <210> SEQ ID NO: 5
236 <211> LENGTH: 19
237 <212> TYPE: DNA
238 <213> ORGANISM: Homo sapiens
240 <400> SEQUENCE: 5
241 tcaggctgca tggttccttg                      19
244 <210> SEQ ID NO: 6
245 <211> LENGTH: 19
246 <212> TYPE: DNA
247 <213> ORGANISM: Homo sapiens
249 <400> SEQUENCE: 6
250 tcctctcagc ggggaagag                      19
253 <210> SEQ ID NO: 7
254 <211> LENGTH: 21
255 <212> TYPE: DNA
256 <213> ORGANISM: Homo sapiens
258 <400> SEQUENCE: 7
259 gacgtgtccc atagtgtttc c                      21
262 <210> SEQ ID NO: 8
263 <211> LENGTH: 18
264 <212> TYPE: DNA
265 <213> ORGANISM: Homo sapiens
267 <400> SEQUENCE: 8
268 tcctgctgcc gtggtgct                      18
271 <210> SEQ ID NO: 9
272 <211> LENGTH: 27
273 <212> TYPE: DNA
274 <213> ORGANISM: Artificial Sequence
276 <220> FEATURE:
277 <223> OTHER INFORMATION: Description of Artificial Sequence:an artificially
synthesized
278     primer sequence
280 <400> SEQUENCE: 9
281 ggggtacctc aggctgcatg ttccttg                      27
284 <210> SEQ ID NO: 10
285 <211> LENGTH: 28
286 <212> TYPE: DNA
287 <213> ORGANISM: Artificial Sequence
289 <220> FEATURE:
290 <223> OTHER INFORMATION: Description of Artificial Sequence:an artificially
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291     primer sequence

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293 <400> SEQUENCE: 10
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298 <211> LENGTH: 29
299 <212> TYPE: DNA
300 <213> ORGANISM: Artificial Sequence
302 <220> FEATURE:
303 <223> OTHER INFORMATION: Description of Artificial Sequence:an artificially
synthesized
304     primer sequence
306 <400> SEQUENCE: 11
307 ggggtaccga cgtgtcccat agtgtttcc                29
310 <210> SEQ ID NO: 12
311 <211> LENGTH: 27
312 <212> TYPE: DNA
313 <213> ORGANISM: Artificial Sequence
315 <220> FEATURE:
316 <223> OTHER INFORMATION: Description of Artificial Sequence:an artificially
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317     primer sequence
319 <400> SEQUENCE: 12
320 ggaagatcctt cctgctgccg tgggtgct                27
323 <210> SEQ ID NO: 13
324 <211> LENGTH: 1159
325 <212> TYPE: DNA
326 <213> ORGANISM: Homo sapiens
328 <400> SEQUENCE: 13
329 tcaggctgca tgttccttgg gtaatgagaa gtcacaatca ctattcatag atgtgtgggg    60
331 agtcactaaa aatatattat tcaactgtcaa tcttagttta tatccagata caacagggtg    120
333 cactgctcctt gtaatggaat cagacttctt attttaacaa gacaaaccaa atccaatcca    180
335 catttgaaga ttataggttt taatataaga aaatgcactc atttctcaaa gaccctagtg    240
337 aagctgtggt taaatgctcc taggtgaacc ccctttgcat ccagtggtc ccaccctgac    300
339 acccagagcc cctacctacc caacacagaa tcatattgctc tgatagaaca atggatccct    360
341 ttttctggaa acattgatgg ccactcctcc cttgtccttg cctatataaa actcctacat    420
343 atattaagag aaaactaagc aagagttttg gaaatctgcc ccaggagact gcatcctgag    480
345 tcacacgcgt ctttgttctc tttcttgtcc caaaaccgtt acctcaagtg acaaatgatc    540
347 aaatctcaaa tatagaattc agggttttac aggtaggcat cttgaggatt tcaaattggt    600
349 aaaagcaact cactcctttt ctactctttg gagagtttca agagcctata gcctctaaaa    660
351 cgcaaatcat tgctaagggt tggggggggag aaaccttttc gaatttttta ggaattcctg    720
353 ctgtttgcct cttcagctac ctacttccta aaaaggatgt atgtcagtgg acagaacagg    780
355 gcaaaacttat tcgaaaaaga aataagaaat aattgccagt gtgtttataa atgatatgaa    840
357 tcaggagtgg tgcgaagagg atagggaaaa aaaaattcta tttggtgctg gaaatactgc    900
359 gctttttttt ttctttttt tttttttctg tgagctggag tgtgccagct ttttcagacg    960
361 gaggaatgct gagtgtcaag gggtcaggat caatccggtg tgagttgatg aggcaggaag   1020
363 gtggggagga atgcgaggaa tgtccctgtt tgtgtaggac tccattcagc tcattggcga   1080
365 gccgcggccg cccggagcgt ataaaagcct cgggccgccc gccccaaact cacacaacaa   1140
367 ctcttccccg ctgagagga                1159
370 <210> SEQ ID NO: 14
371 <211> LENGTH: 355
372 <212> TYPE: DNA
373 <213> ORGANISM: Homo sapiens

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/516,517

DATE: 12/10/2004

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Input Set : A:\Q85059.txt

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date